



1600

145 ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/911,826A

DATE: 03/07/2002

TIME: 15:13:40

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\I911826A.raw

3 <110> APPLICANT: Rotin, Daniela and Pham, Nam
 5 <120> TITLE OF INVENTION: RAS Activator Nucleic Acid Molecules, Polypeptides and
 6 Methods of Use
 8 <130> FILE REFERENCE: DDW-5001-US
 10 <140> CURRENT APPLICATION NUMBER: 09/911,826A
 C--> 11 <141> CURRENT FILING DATE: 2002-02-26
 13 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00042
 14 <151> PRIOR FILING DATE: 2000-01-20
 16 <150> PRIOR APPLICATION NUMBER: 2,259,830
 17 <151> PRIOR FILING DATE: 1999-01-20
 19 <160> NUMBER OF SEQ ID NOS: 27
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 6568
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (63)..(4562)
 32 <400> SEQUENCE: 1
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 35 tt atg aaa cca cta gca atc cca gct aac cat gga gtt atg ggc cag 107
 36 Met Lys Pro Leu Ala Ile Pro Ala Asn His Gly Val Met Gly Gln
 37 1 5 10 15
 39 cag gag aaa cac tca ctt cct gca gat ttc aca aaa ctg cat ctt act 155
 40 Gln Glu Lys His Ser Leu Pro Ala Asp Phe Thr Lys Leu His Leu Thr
 41 20 25 30
 43 gac agt ctc cac cca cag gtg acc cac gtt tct tct agc cat tca gga 203
 44 Asp Ser Leu His Pro Gln Val Thr His Val Ser Ser His Ser Gly
 45 35 40 45
 47 tgt agt atc act agt gat tct ggg agc agc agt ctt tct gat atc tac 251
 48 Cys Ser Ile Thr Ser Asp Ser Gly Ser Ser Leu Ser Asp Ile Tyr
 49 50 55 60
 51 cag gcc aca gaa agc gag gct ggt gat atg gac ctg agt ggg ttg cca 299
 52 Gln Ala Thr Glu Ser Glu Ala Gly Asp Met Asp Leu Ser Gly Leu Pro
 53 65 70 75
 55 gaa aca gca gtg gat tcc gaa gac gac gat gaa gaa gac att gag 347
 56 Glu Thr Ala Val Asp Ser Glu Asp Asp Asp Glu Asp Ile Glu
 57 80 85 90 95
 59 aga gca tca gat cct ctg atg agc agg gac att gtg aga gac tgc cta 395
 60 Arg Ala Ser Asp Pro Leu Met Ser Arg Asp Ile Val Arg Asp Cys Leu
 61 100 105 110
 63 gag aag gac cca att gac cgg aca gat gat gac att gaa caa ctc ttg 443

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64	Glu Lys Asp Pro Ile Asp Arg Thr Asp Asp Asp Ile Glu Gln Leu Leu			
65	115	120	125	
67	gaa ttt atg cac cag ttg cct gct ttt gcc aat atg aca atg tca gtg	491		
68	Glu Phe Met His Gln Leu Pro Ala Phe Ala Asn Met Thr Met Ser Val			
69	130	135	140	
71	agg cga gaa ctc tgt gct gtg atg gtg ttc gca gtg gtg gaa aga gca	539		
72	Arg Arg Glu Leu Cys Ala Val Met Val Phe Ala Val Val Glu Arg Ala			
73	145	150	155	
75	ggg acc ata gtg tta aat gat ggt gaa gag ctg gac tcc tgg tca gtg	587		
76	Gly Thr Ile Val Leu Asn Asp Gly Glu Glu Leu Asp Ser Trp Ser Val			
77	160	165	170	175
79	att ctc aat gga tct gtg gaa gtg act tat cca gat gga aaa gca gaa	635		
80	Ile Leu Asn Gly Ser Val Glu Val Thr Tyr Pro Asp Gly Lys Ala Glu			
81	180	185	190	
83	ata ctg tgc atg gga aat agt ttt ggt gtc tct cct acc atg gac aaa	683		
84	Ile Leu Cys Met Gly Asn Ser Phe Gly Val Ser Pro Thr Met Asp Lys			
85	195	200	205	
87	gaa tac atg aaa gga gtg atg aga aca aag gtg gat gac tgc cag ttt	731		
88	Glu Tyr Met Lys Gly Val Met Arg Thr Lys Val Asp Asp Cys Gln Phe			
89	210	215	220	
91	gtc tgc ata gcc cag caa gat tac tgc cgt att ctc aat caa gta gaa	779		
92	Val Cys Ile Ala Gln Gln Asp Tyr Cys Arg Ile Leu Asn Gln Val Glu			
93	225	230	235	
95	aag aac atg caa aaa gtt gaa gag gaa gga gag att gtt atg gtg aaa	827		
96	Lys Asn Met Gln Lys Val Glu Glu Gly Glu Ile Val Met Val Lys			
97	240	245	250	255
99	gaa cac cga gaa ctt gat cga act gga aca aga aag gga cac att gtc	875		
100	Glu His Arg Glu Leu Asp Arg Thr Gly Thr Arg Lys Gly His Ile Val			
101	260	265	270	
103	atc aag ggt acc tca gaa agg tta aca atg cat ttg gtg gaa gag cat	923		
104	Ile Lys Gly Thr Ser Glu Arg Leu Thr Met His Leu Val Glu Glu His			
105	275	280	285	
107	tca gta gta gat cca aca ttc ata gaa gac ttt ctg ttg acc tat agg	971		
108	Ser Val Val Asp Pro Thr Phe Ile Glu Asp Phe Leu Leu Thr Tyr Arg			
109	290	295	300	
111	act ttt ctt tct agc cca atg gaa gtg ggc aaa aag tta ttg gag tgg	1019		
112	Thr Phe Leu Ser Ser Pro Met Glu Val Gly Lys Lys Leu Leu Glu Trp			
113	305	310	315	
115	ttt aat gac ccg agc ctc agg gat aag gtt aca cgg gta gta tta ttg	1067		
116	Phe Asn Asp Pro Ser Leu Arg Asp Lys Val Thr Arg Val Val Leu Leu			
117	320	325	330	335
119	tgg gta aat aat cac ttc aat gac ttt gaa gga gat cct gca atg act	1115		
120	Trp Val Asn Asn His Phe Asn Asp Phe Glu Gly Asp Pro Ala Met Thr			
121	340	345	350	
123	cga ttt tta gaa gaa ttt gaa aac aat ctg gaa aga gag aaa atg ggt	1163		
124	Arg Phe Leu Glu Glu Phe Glu Asn Asn Leu Glu Arg Glu Lys Met Gly			
125	355	360	365	
127	gga cac cta agg ctg ttg aat atc gcg tgt gct gct aaa gca aaa aga	1211		
128	Gly His Leu Arg Leu Leu Asn Ile Ala Cys Ala Ala Lys Ala Lys Arg			

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129	370	375	380	
131	aga ttg atg acg tta aca aaa cca tcc cga gaa gct cct ttg cct ttt			1259
132	Arg Leu Met Thr Leu Thr Lys Pro Ser Arg Glu Ala Pro Leu Pro Phe			
133	385	390	395	
135	atc tta ctt gga ggc tct gag aag gga ttt gga atc ttt gtt gac agt			1307
136	Ile Leu Leu Gly Gly Ser Glu Lys Gly Phe Gly Ile Phe Val Asp Ser			
137	400	405	410	415
139	gta gat tca ggt agc aaa gca act gaa gca ggc ttg aaa cgg ggg gat			1355
140	Val Asp Ser Gly Ser Lys Ala Thr Glu Ala Gly Leu Lys Arg Gly Asp			
141	420	425	430	
143	cag ata tta gaa gta aat ggc caa aac ttt gaa aac att cag ctg tca			1403
144	Gln Ile Leu Glu Val Asn Gly Gln Asn Phe Glu Asn Ile Gln Leu Ser			
145	435	440	445	
147	aaa gct atg gaa att ctt aga aat aac aca cat tta tct atc act gtg			1451
148	Lys Ala Met Glu Ile Leu Arg Asn Asn Thr His Leu Ser Ile Thr Val			
149	450	455	460	
151	aaa acc aat tta ttt gta ttt aaa gaa ctt cta aca aga ttg tca gaa			1499
152	Lys Thr Asn Leu Phe Val Phe Lys Glu Leu Leu Thr Arg Leu Ser Glu			
153	465	470	475	
155	gag aaa aga aat ggt gcc ccc cac ctt cct aaa att ggt gac att aaa			1547
156	Glu Lys Arg Asn Gly Ala Pro His Leu Pro Lys Ile Gly Asp Ile Lys			
157	480	485	490	495
159	aag gcc agt cgc tac tcc att cca gat ctt gct gta gat gta gaa cag			1595
160	Lys Ala Ser Arg Tyr Ser Ile Pro Asp Leu Ala Val Asp Val Glu Gln			
161	500	505	510	
163	gtg ata gga ctt gaa aaa gtg aac aaa aaa agt aaa gcc aac act gtg			1643
164	Val Ile Gly Leu Glu Lys Val Asn Lys Lys Ser Lys Ala Asn Thr Val			
165	515	520	525	
167	gga gga agg aac aag ctg aaa aag ata ctc gac aag act cgg atc agt			1691
168	Gly Gly Arg Asn Lys Leu Lys Ile Leu Asp Lys Thr Arg Ile Ser			
169	530	535	540	
171	atc ttg cca cag aaa cca tac aat gat att ggg att ggt cag tct caa			1739
172	Ile Leu Pro Gln Lys Pro Tyr Asn Asp Ile Gly Ile Gly Gln Ser Gln			
173	545	550	555	
175	gat gac agc ata gta gga tta agg cag aca aag cac atc cca act gca			1787
176	Asp Asp Ser Ile Val Gly Leu Arg Gln Thr Lys His Ile Pro Thr Ala			
177	560	565	570	575
179	ttg cct gtc agt gga acc tta tca tcc agt aat cct gat tta ttg cag			1835
180	Leu Pro Val Ser Gly Thr Leu Ser Ser Asn Pro Asp Leu Leu Gln			
181	580	585	590	
183	tca cat cat cgc att tta gac ttc agt gct act cct gac ttg cca gat			1883
184	Ser His His Arg Ile Leu Asp Phe Ser Ala Thr Pro Asp Leu Pro Asp			
185	595	600	605	
187	caa gtg cta agg gtt ttt aag gct gat cag caa agc cgc tac atc atg			1931
188	Gln Val Leu Arg Val Phe Lys Ala Asp Gln Gln Ser Arg Tyr Ile Met			
189	610	615	620	
191	atc agt aag gac act aca gca aag gaa gtg gtc att cag gct atc agg			1979
192	Ile Ser Lys Asp Thr Thr Ala Lys Glu Val Val Ile Gln Ala Ile Arg			
193	625	630	635	

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195	gag	ttt	gct	gtt	act	gcc	acc	ccg	gat	caa	tat	tca	cta	tgt	gag	gtc		2027
196	Glu	Phe	Ala	Val	Thr	Ala	Thr	Pro	Asp	Gln	Tyr	Ser	Leu	Cys	Glu	Val		
197	640				645					650						655		
199	tct	gtc	aca	cct	gag	gga	gta	atc	aaa	caa	aga	aga	ctt	cca	gat	cag		2075
200	Ser	Val	Thr	Pro	Glu	Gly	Val	Ile	Lys	Gln	Arg	Arg	Leu	Pro	Asp	Gln		
201					660				665							670		
203	ctt	tcc	aaa	ctt	gca	gac	aga	ata	caa	ctg	agt	gga	agg	tat	tat	ctg		2123
204	Leu	Ser	Lys	Leu	Ala	Asp	Arg	Ile	Gln	Leu	Ser	Gly	Arg	Tyr	Tyr	Leu		
205					675				680							685		
207	aaa	aac	aac	atg	gaa	aca	gaa	act	ctt	tgt	tca	gat	gaa	gat	gct	cag		2171
208	Lys	Asn	Asn	Met	Glu	Thr	Glu	Thr	Leu	Cys	Ser	Asp	Glu	Asp	Ala	Gln		
209					690				695							700		
211	gag	ttg	ttg	aga	gag	agt	caa	att	tcc	ctc	ctt	cag	ctc	agc	act	gtg		2219
212	Glu	Leu	Leu	Arg	Glu	Ser	Gln	Ile	Ser	Leu	Leu	Gln	Leu	Ser	Thr	Val		
213					705				710							715		
215	gaa	gtt	gca	aca	cag	ctc	tct	atg	cga	aat	ttt	gaa	ctc	ttt	cgc	aac		2267
216	Glu	Val	Ala	Thr	Gln	Leu	Ser	Met	Arg	Asn	Phe	Glu	Leu	Phe	Arg	Asn		
217					720				725							730		735
219	att	gaa	cct	act	gaa	tat	ata	gat	gat	tta	ttt	aaa	ctc	aga	tca	aaa		2315
220	Ile	Glu	Pro	Thr	Glu	Tyr	Ile	Asp	Asp	Leu	Phe	Lys	Leu	Arg	Ser	Lys		
221					740				745							750		
223	acc	agc	tgt	gcc	aac	ctg	aag	aga	ttt	gaa	gaa	gtc	att	aac	cag	gaa		2363
224	Thr	Ser	Cys	Ala	Asn	Leu	Lys	Arg	Phe	Glu	Glu	Val	Ile	Asn	Gln	Glu		
225					755				760							765		
227	aca	ttt	tgg	gta	gca	tct	gaa	att	ctc	aga	gaa	aca	aac	cag	ctg	aag		2411
228	Thr	Phe	Trp	Val	Ala	Ser	Glu	Ile	Leu	Arg	Glu	Thr	Asn	Gln	Leu	Lys		
229					770				775							780		
231	agg	atg	aag	atc	att	aag	cat	ttc	atc	aag	ata	gca	ctg	cac	tgt	agg		2459
232	Arg	Met	Lys	Ile	Ile	Lys	His	Phe	Ile	Lys	Ile	Ala	Leu	His	Cys	Arg		
233					785				790							795		
235	gaa	tgc	aag	aat	ttt	aac	tca	atg	ttt	gca	atc	atc	agt	ggc	cta	aac		2507
236	Glu	Cys	Lys	Asn	Phe	Asn	Ser	Met	Phe	Ala	Ile	Ile	Ser	Gly	Leu	Asn		
237					800				805							810		815
239	ctg	gca	cca	gtg	gca	aga	ctg	cga	acg	acc	tgg	gag	aaa	ctt	ccc	aat		2555
240	Leu	Ala	Pro	Val	Ala	Arg	Leu	Arg	Thr	Thr	Trp	Glu	Lys	Leu	Pro	Asn		
241					820				825							830		
243	aaa	tac	gaa	aaa	cta	ttt	caa	gat	ctc	caa	gac	ctg	ttt	gat	cct	tcc		2603
244	Lys	Tyr	Glu	Lys	Leu	Phe	Gln	Asp	Leu	Gln	Asp	Leu	Phe	Asp	Pro	Ser		
245					835				840							845		
247	aga	aac	atg	gca	aaa	tat	cgt	aat	gtt	ctc	aat	agt	caa	aat	cta	caa		2651
248	Arg	Asn	Met	Ala	Lys	Tyr	Arg	Asn	Val	Leu	Asn	Ser	Gln	Asn	Leu	Gln		
249					850				855							860		
251	cct	ccc	ata	atc	cct	cta	ttc	cca	gtt	atc	aaa	aag	gat	ctc	acc	ttc		2699
252	Pro	Pro	Ile	Ile	Pro	Leu	Phe	Pro	Val	Ile	Lys	Lys	Asp	Leu	Thr	Phe		
253					865				870							875		
255	ctt	cac	gaa	gga	aat	gac	tca	aaa	gta	gac	ggg	ctg	gtc	aat	ttt	gag		2747
256	Leu	His	Glu	Gly	Asn	Asp	Ser	Lys	Val	Asp	Gly	Leu	Val	Asn	Phe	Glu		
257					880				885							890		895
259	aag	cta	agg	atg	att	gca	aaa	gaa	att	cgt	cac	gtt	ggc	cga	atg	gct		2795

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260	Lys Leu Arg Met Ile Ala Lys Glu Ile Arg His Val Gly Arg Met Ala			
261	900	905	910	
263	tca gtg aac atg gac cct gcc ctc atg ttc agg act cgg aag aag aaa	2843		
264	Ser Val Asn Met Asp Pro Ala Leu Met Phe Arg Thr Arg Lys Lys Lys			
265	915	920	925	
267	tgg cgg agt ttg ggg tct ctc agc cag ggt agt aca aat gca aca gtg	2891		
268	Trp Arg Ser Leu Gly Ser Leu Ser Gln Gly Ser Thr Asn Ala Thr Val			
269	930	935	940	
271	cta gat gtt gct cag aca ggt ggt cat aaa aag cgg gta cgt cgt agt	2939		
272	Leu Asp Val Ala Gln Thr Gly Gly His Lys Lys Arg Val Arg Arg Ser			
273	945	950	955	
275	tcc ttt ctc aat gcc aaa aag ctt tat gaa gat gcc caa atg gct cga	2987		
276	Ser Phe Leu Asn Ala Lys Lys Leu Tyr Glu Asp Ala Gln Met Ala Arg			
277	960	965	970	975
279	aaa gtg aag cag tac ctt tcc aat ttg gag cta gaa atg gac gag gag	3035		
280	Lys Val Lys Gln Tyr Leu Ser Asn Leu Glu Leu Glu Met Asp Glu Glu			
281	980	985	990	
283	agt ctt cag aca tta tct ctg cag tgt gag cca gca acc aac aca ttg	3083		
284	Ser Leu Gln Thr Leu Ser Leu Gln Cys Glu Pro Ala Thr Asn Thr Leu			
285	995	1000	1005	
287	cct aag aat cct ggt gac aaa aag cct gtc aaa tcc gag acc tct cca	3131		
288	Pro Lys Asn Pro Gly Asp Lys Lys Pro Val Lys Ser Glu Thr Ser Pro			
289	1010	1015	1020	
291	gta gct cca agg gca ggg tca caa cag aaa gct cag tcc ctg cca cag	3179		
292	Val Ala Pro Arg Ala Gly Ser Gln Gln Lys Ala Gln Ser Leu Pro Gln			
293	1025	1030	1035	
295	ccc cag cag cag cca cca gca cat aaa atc aac cag gga cta cag	3227		
296	Pro Gln Gln Gln Pro Pro Ala His Lys Ile Asn Gln Gly Leu Gln			
297	1040	1045	1050	1055
299	gtt ccc gcc gtg tcc ctt tat cct tca cgg aag aaa gtg ccc gta aag	3275		
300	Val Pro Ala Val Ser Leu Tyr Pro Ser Arg Lys Lys Val Pro Val Lys			
301	1060	1065	1070	
303	gat ctc cca cct ttt ggc ata aac tct cca caa gct tta aaa aaa att	3323		
304	Asp Leu Pro Pro Phe Gly Ile Asn Ser Pro Gln Ala Leu Lys Lys Ile			
305	1075	1080	1085	
307	ctt tct ttg tct gaa gaa gga agt ttg gaa cgt cac aag aaa cag gct	3371		
308	Leu Ser Leu Ser Glu Glu Gly Ser Leu Glu Arg His Lys Lys Gln Ala			
309	1090	1095	1100	
311	gaa gat aca ata tca aat gca tct tcg cag ctt tct cct cct act	3419		
312	Glu Asp Thr Ile Ser Asn Ala Ser Ser Gln Leu Ser Ser Pro Pro Thr			
313	1105	1110	1115	
315	tct cca cag agt tct cca agg aaa ggc tat act ttg gct ccc agt ggt	3467		
316	Ser Pro Gln Ser Ser Pro Arg Lys Gly Tyr Thr Leu Ala Pro Ser Gly			
317	1120	1125	1130	1135
319	act gtg gat aat ttt tca gat tct ggt cac agt gaa att tct tca cga	3515		
320	Thr Val Asp Asn Phe Ser Asp Ser Gly His Ser Glu Ile Ser Ser Arg			
321	1140	1145	1150	
323	tcc agt att gtt agc aat tcg tct ttt gac tca gtg cca gtc tca ctg	3563		
324	Ser Ser Ile Val Ser Asn Ser Ser Phe Asp Ser Val Pro Val Ser Leu			

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 203,227,239,271,279
Seq#:5; Xaa Pos. 16,18,45,59,61,151,166,215
Seq#:6; Xaa Pos. 1,35,123,178,239
Seq#:15; Xaa Pos. 50

VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs. Replaced Current Filing Date
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:192
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:224
L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:256
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:272
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16
L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:32
L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:48
L:803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:144
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:160
L:815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:208
L:836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:32
L:857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:112
L:869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:176
L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:224
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48